

FIG. 1A

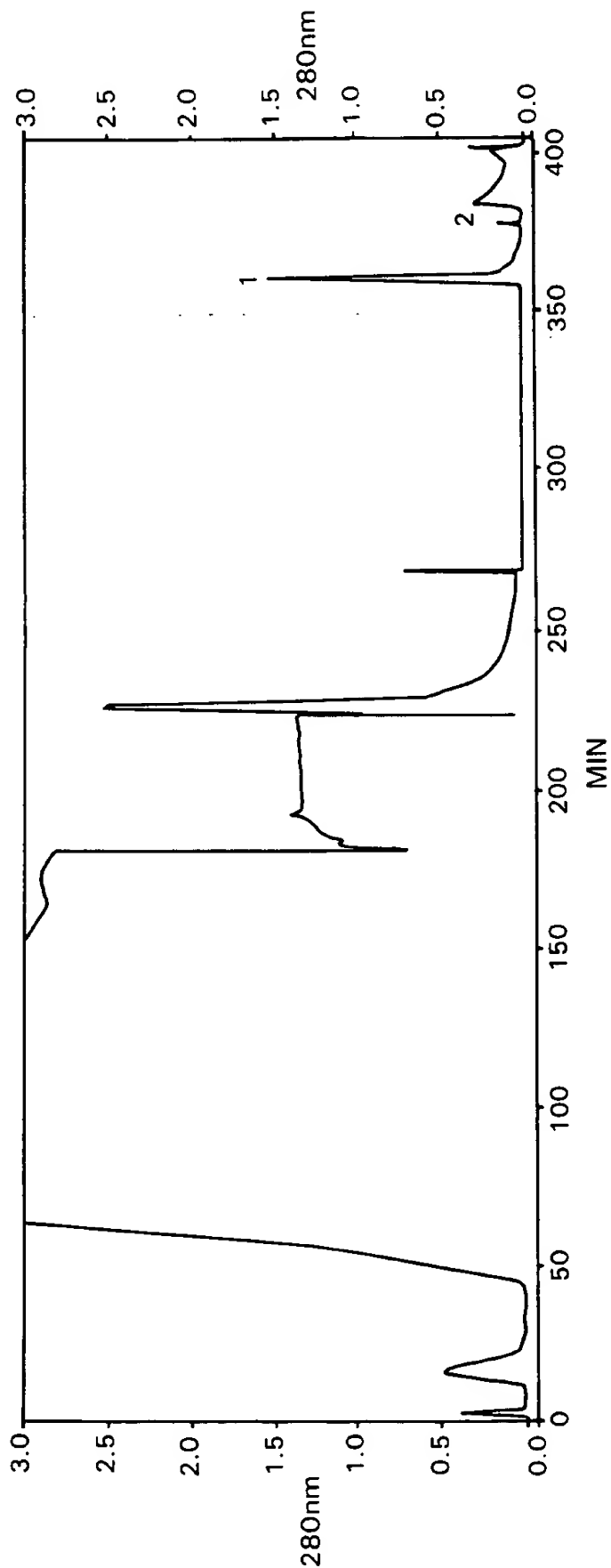


FIG. 1B

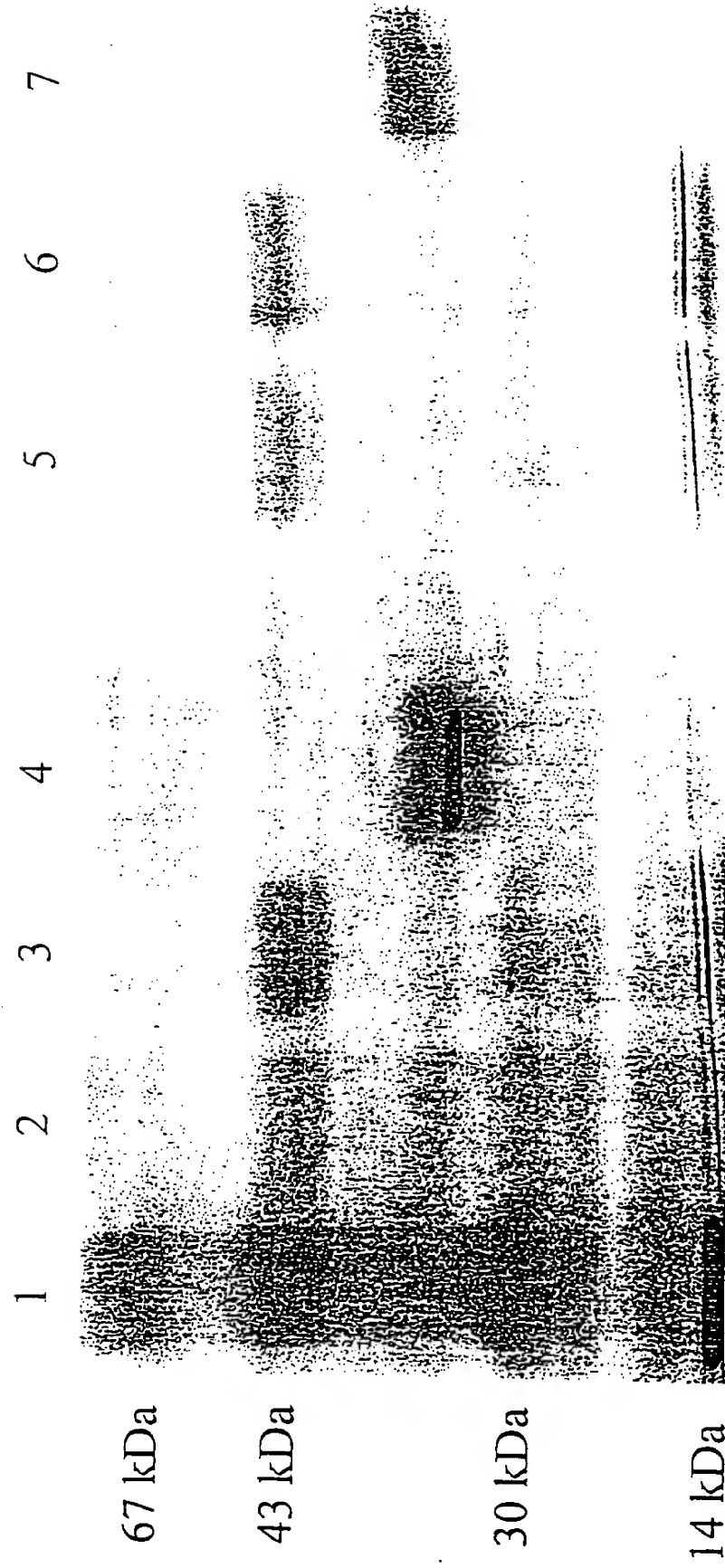


FIG. 2

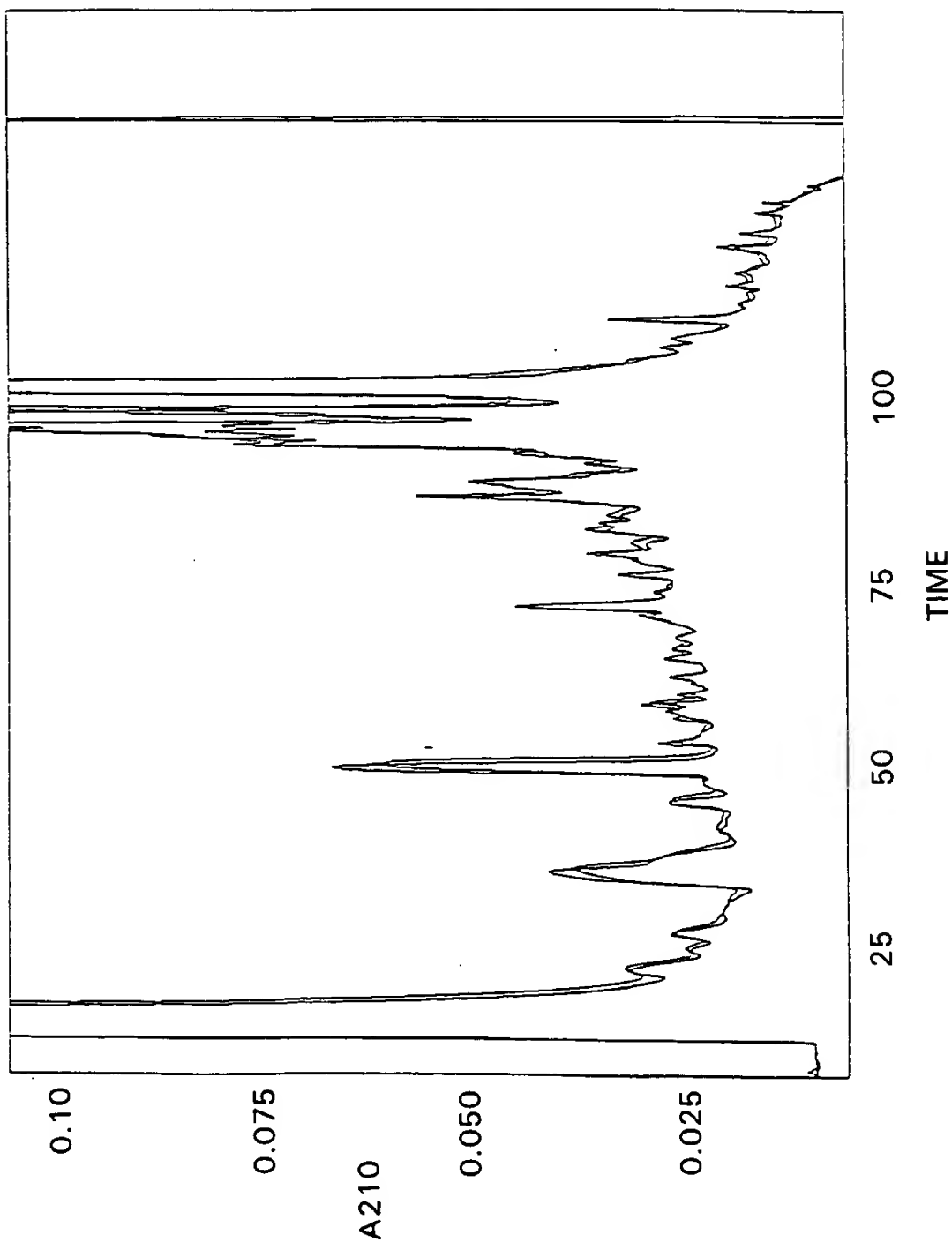
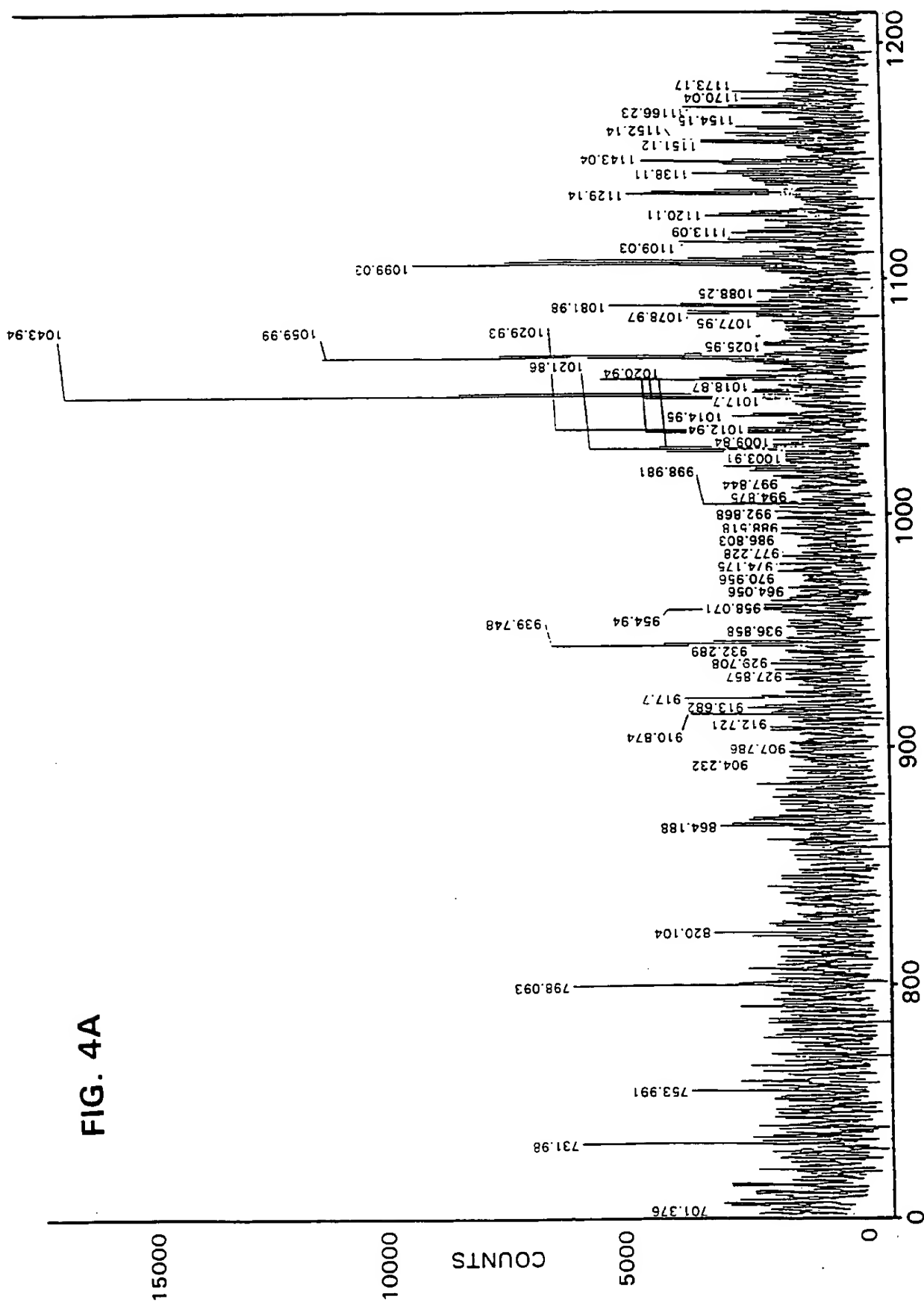


FIG. 3



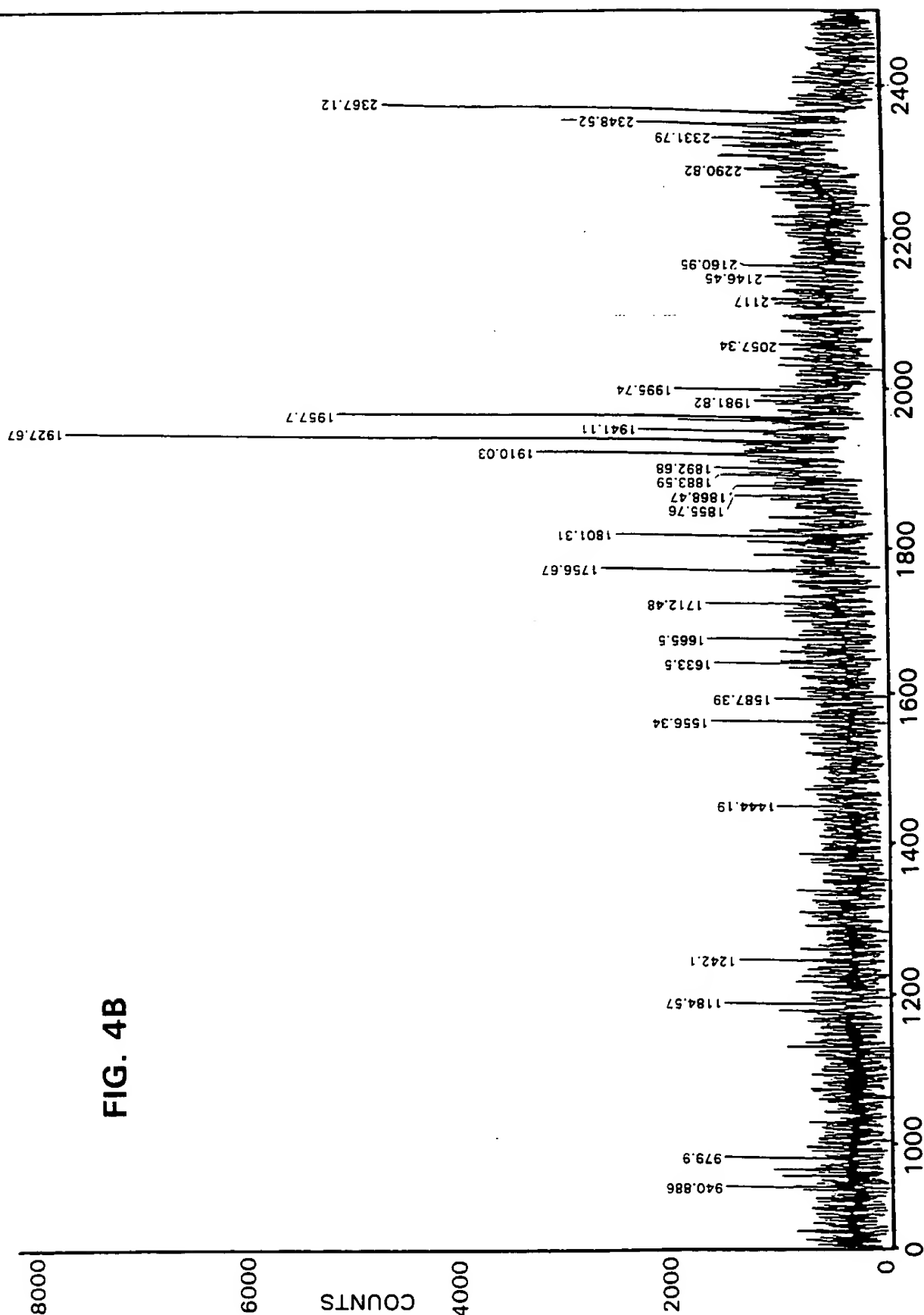
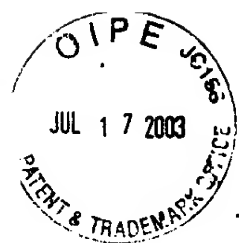
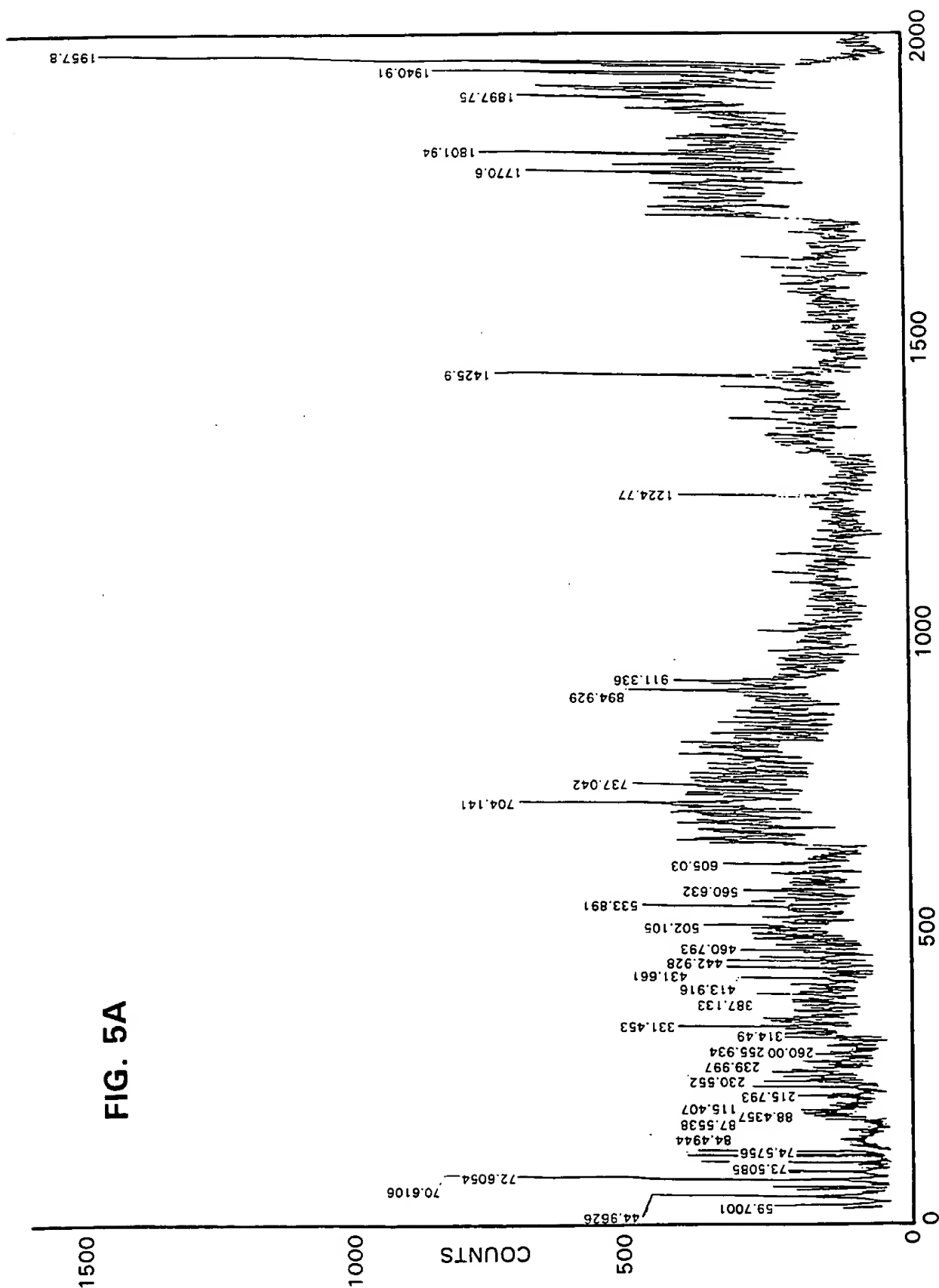




FIG. 5A





Sample ID (comment): R4A3F37m1957
Database searched: NCBI nr. 7.5.97
Molecular weight search (1000-100000 Da) selects 269572 entries.
Species search (HOMO SAPIENS) selects 22771 entries.
Combined molecular weight and species searches select 20933 entries.
Number of sequences passing through parent mass filter: 84015
search selects 257 entries
Ion Types Considered: a b y n h l

| Result Summary | | | | | | | | | |
|----------------|-----------------------|-----------------------------------|-----------------|-------------------------|----------------------------------|---------------------------------|-------------------------------------|-------------------------|--|
| Search Mode | Max. # Unmatched Ions | Peptide Masses are Par(m)Frag(av) | Digest Used | Max. # Missed Cleavages | Cysteines Modified by unmodified | Peptide N terminus Hydrogen (H) | Peptide C terminus Free Acid (O II) | Sequence | Protein Name |
| Identity | 5 | | No enzyme | 1 | | | | | |
| Rank | MS-Digest Index# | NCBI nr. 7.597 Accession# | Protein MW (Da) | Species | Calculated MH+ (Da) | MH+ Error (Da) | Unmatched Ions | Sequence | Protein Name |
| 1 | 240839 | 1839795 | 21251.4 | HOMO SAPIENS | 1956.9052 | 0.2948 | 2 | (Y)VDDTQFVRFDSDAASQR(M) | (D82930) HLA-A26-variant |
| 1 | 152874 | 915219 | 40679.8 | HOMO SAPIENS | 1956.9052 | 0.2948 | 2 | (Y)VDDTQFVRFDSDAASQR(M) | (U25971) MHC class 1 antigen HLA-A2407 |
| 1 | 141923 | 825673 | 20921.2 | HOMO SAPIENS | 1956.9052 | 0.2948 | 2 | (Y)VDDTQFVRFDSDAASQR(M) | (X82161) HLA-A alpha1 and alpha2 domains |
| 1 | 159176 | 994765 | 41113.1 | HOMO SAPIENS | 1956.9052 | 0.2948 | 2 | (Y)VDDTQFVRFDSDAASQR(M) | (D32129) HLA-A26 |
| 1 | 282322 | 250934 | 38703.4 | HOMO SAPIENS | 1956.9052 | 0.2948 | 2 | (Y)VDDTQFVRFDSDAASQR(M) | (Z97370) human leukocyte antigen |
| 1 | 133479 | 717123 | 40895.1 | HOMO SAPIENS | 1956.9052 | 0.2948 | 2 | (Y)VDDTQFVRFDSDAASQR(M) | (U18930)MHC class 1 antigen HLA-A2 |
| 1 | 49436 | 785055 | 38355.8 | HOMO SAPIENS | 1956.9052 | 0.2948 | 2 | (Y)VDDTQFVRFDSDAASQR(M) | (M160010) HLA-AH class 1 antigen (AA at 30) |
| 1 | 277806 | 2394324 | 10423.4 | HOMO SAPIENS | 1956.9052 | 0.2948 | 2 | (Y)VDDTQFVRFDSDAASQR(M) | (AF017310) MHC class 1 antigen |
| 1 | 277805 | 2394322 | 10430.3 | HOMO SAPIENS | 1956.9052 | 0.2948 | 2 | (Y)VDDTQFVRFDSDAASQR(M) | (AF017309) MHC class 1 antigen |
| 1 | 277713 | 2394009 | 21027.3 | HOMO SAPIENS | 1956.9052 | 0.2948 | 2 | (Y)VDDTQFVRFDSDAASQR(M) | (AF012767) MHC class 1 antigen HLA-A heavy chain |

FIG. 5B



gb/AA548636/AA548636.nj.38d02.s1.NCI.CCAP.AAL.Homo.Sapiens.cDNA.clone IMAGE 994755 similar to gb:z46633.HLA.CLASS.I.HISTOCOMPATIBILITY ANTIGEN, A-2 A*0201 ALPHA (HUMAN);
Length = 539

Plus Strand HSPs:

Score = 30 (41.9 bits), Expect = 8.1e-05, P = 8.1e-05
Identities = 18/18 (100%), Positives = 18/18 (100%), Frame = +2

Query: 1 VDDTQFVRFSDAASQRM 18
VDDTQFVRFSDAASQRM
Sbjct: 152 VDDTQFVRFSDAASQRM 205

gb/AA147151/AA147151.zo32d06.r1.Stratagene.colon.(#937204).Homo.sapiens.cDNA.clone 5885875 similar to gb:M64740.HLA.CLASS.I.HISTOCOMPATIBILITY ANTIGEN, A-24 (A-9) A*2402 ALPHA (HUMAN);
Length = 581

Plus Strands HSPs:

Score = 90 (41.9 bits), Expect = 8.1e-05, P = 8.1e-05
Identities = 18/18 (100%), Positives = 18/18 (100%), Frame = +1

Query: 1 VDDTQFVRFSDAASQRM 18
VDDTQFVRFSDAASQRM
13 VDDTQFVRFSDAASQRM 66

gb/H23377/H23377.yf57e02.r1.Homo.sapiens.cDNA.clone 52227 5'similar to gb:X00492.cd51.HLA.CLASS.I.HISTOCOMPATIBILITY ANTIGEN, A-3A A*0301 ALPHA (HUMAN);
Length = 459

Plus Strand HSPs:

Score = 90 (41.9 bits), Expect = 8.1e-05, P = 8.1e-05
Identities = 18/18 (100%), Positives = 18/18 (100%), Frame = +1

Query: 1 VDDTQFVRFSDAASQRM 18
VDDTQFVRFSDAASQRM
Sbjct: 154 VDDTQFVRFSDAASQRM 207

gb/R13904/R13904.yf62c03.r1.Homo.sapiens.cDNA.clone 26801 5'similar to gb:M64742.cd51.HLA.CLASS.I.HISTOCOMPATIBILITY ANTIGEN, A-23(A-9) A*2301 (HUMAN);
Length = 459

Plus Strand HSPs:

Score 90 (41.9 bits), Expect = 8.1e-05 P=8.1e-05
Identities = 18/18 (100%), Positives = 18/18 (100%), Frame = +2

Query: 1 VDDTQFVRFSDAASQRM 18
VDDTQFVRFSDAASQRM
Sbjct: 146 VDDTQFVRFSDAASQRM 199

gb/R12066/R12066.yf54d10.r1.Homo.sapiens.cDNA.clone 26062 5'similar to gb:X00492.cd51.HLA.CLASS.I.HISTOCOMPATIBILITY ANTIGEN, A-3A*0301 alpha (human);
Length = 405

Plus Strand HSPs:

Score = 90 (41.9 bits), Expect = 8.1e-05, P = 8.1e-05
Identities = 18/18 (100%), Positives = 18/18 (100%), Frame = +2

Query: 1 VDDTQFVRFSDAASQRM 18
VDDTQFVRFSDAASQRM
Sbjct: 158 VDDTQFVRFSDAASQRM 211

gb/AA132653/AA132653.zo21a05.r1.Stratagene.colon.(#937204).Homo.sapiens.cDNA.clone 587504 5' similar to gb:z46633.HLA.CLASS.I.HISTOCOMPATIBILITY ANTIGEN, A-2 A* 0201 ALPHA (HUMAN);
Length = 428

Plus Strand HSPs:

Score = 90 (41.9 bits), Expect = 8.1e-05, P = 8.1e-05
Identities = 18/18 (100%), Positives = 18/18 (100%), Frame = +3

Query: 1 VDDTQFVRFSDAASQRM 18
VDDTQFVRFSDAASQRM
Sbjct: 158 VDDTQFVRFSDAASQRM 203

gb/R59764/R59764.yh07c05.r1.Homo.sapiens.cDNA.clone 42563 5'similar to gb:X00492.cd51.HLA.CLASS.I.HISTOCOMPATIBILITY ANTIGEN, A-3 A* 0301 ALPHA (HUMAN);
Length = 461

Plus Strands HSPs:

Score = 90 (41.9 bits), Expect = 8.1e-05, P = 8.1e-05
Identities = 18/18 (100%), Positives = 18/18 (100%), Frame = +1

Query: 1 VDDTQFVRFSDAASQRM 18
VDDTQFVRFSDAASQRM
138 VDDTQFVRFSDAASQRM 210

gb/AA489534/AA489534.ab37f08.r1.Stratagene.HeLa.cell.s3.937216.Homo.sapiens.cDNA.clone 843015 5' similar to gb:L06425.HLA.CLASS.I.HISTOCOMPATIBILITY ANTIGEN, AW-34(A-10) A*3402 ALPHA (HUMAN);
Length = 478

Plus Strand HSPs:

Score = 90 (41.9 bits), Expect = 8.1e-05, P = 8.1e-05
Identities = 18/18 (100%), Positives = 18/18 (100%), Frame = +3

Query: 1 VDDTQFVRFSDAASQRM 18
VDDTQFVRFSDAASQRM
Sbjct: 138 VDDTQFVRFSDAASQRM 191

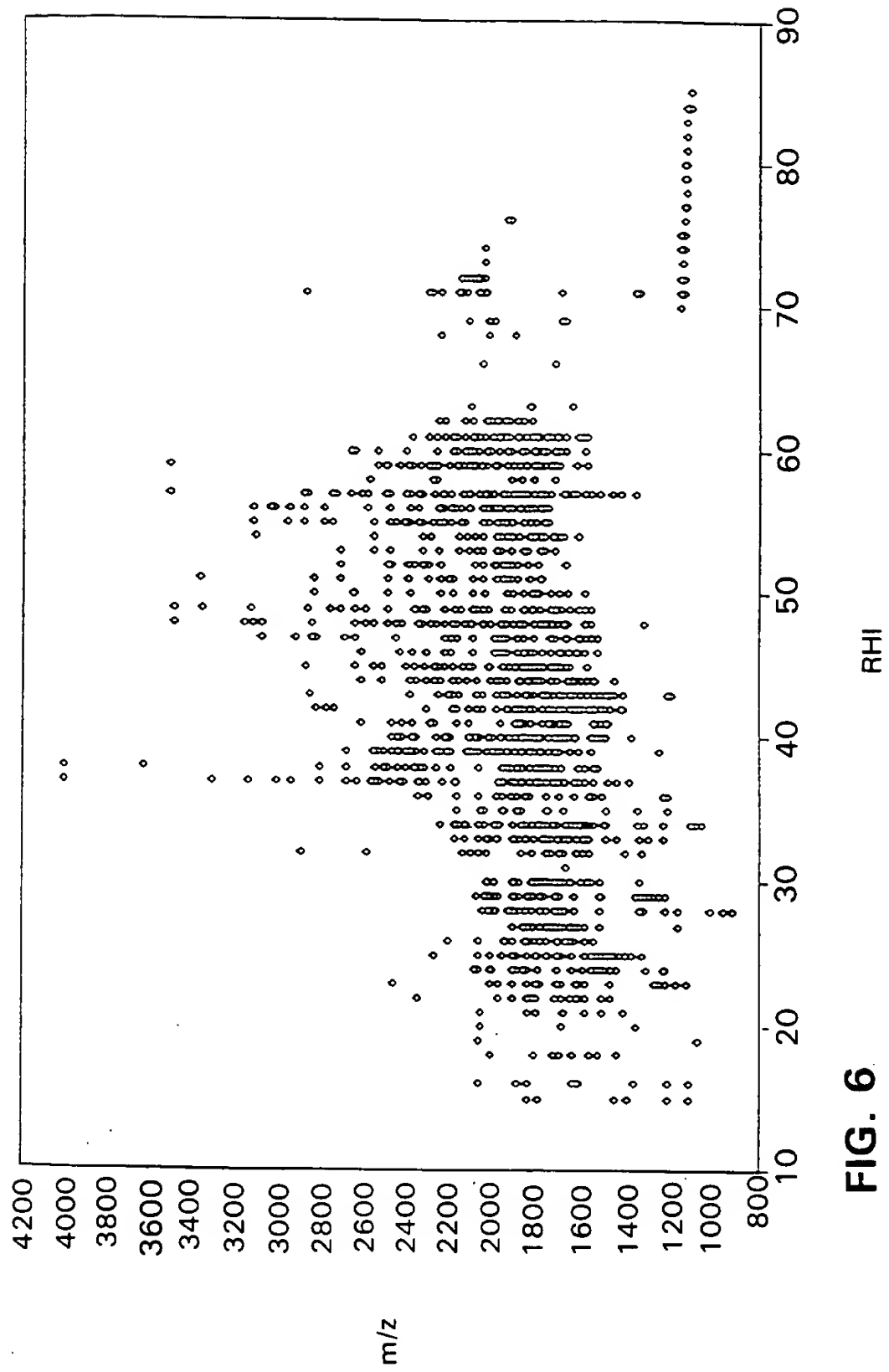


FIG. 6